

10/563194

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SEQUENCE LISTING

<110> JENSEN, Jens Stougaard
<110> MADSEN, Lene Heegaard
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<110> SANDAL, Niels Norgaard

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Tyr Ala Asn Leu Thr Thr Val Asp Leu Leu Lys Arg Phe Asn Ser Tyr
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Thr Tyr Pro Ile Arg Pro Gly Asp Thr Leu Gln Asp Ile Ala Asn Gln
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Tyr Lys Asn Gly
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Val Tyr Val Pro Leu Tyr His Arg
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Lys Thr Ala Ile Lys Lys Met Asp Val Gln Ala Ser Thr Glu
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9395

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Leu Phe Ser Arg
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9662

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Leu His Asn Gly Glu Leu
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9764

Val Gln Glu Ile Ile His Cys Asp Gln Val Asp Leu Leu
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Leu Pro Thr Lys Val Lys Leu Ser Ile Tyr Cys Leu Asp
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<212> PRT
<213> Lotus japonicus Gifu

<400> 24

Met Lys Leu Lys Thr Gly Leu Leu Leu Phe Phe Ile Leu Leu Leu Gly
1 5 10 15

His Val Cys Phe His Val Glu Ser Asn Cys Leu Lys Gly Cys Asp Leu
20 25 30

Ala Leu Ala Ser Tyr Tyr Ile Leu Pro Gly Val Phe Ile Leu Gln Asn
35 40 45

Ile Thr Thr Phe Met Gln Ser Glu Ile Val Ser Ser Asn Asp Ala Ile
50 55 60

Thr Ser Tyr Asn Lys Asp Lys Ile Leu Asn Asp Ile Asn Ile Gln Ser
65 70 75 80

Phe Gln Arg Leu Asn Ile Pro Phe Pro Cys Asp Cys Ile Gly Gly Glu
85 90 95

Phe Leu Gly His Val Phe Glu Tyr Ser Ala Ser Lys Gly Asp Thr Tyr
100 105 110

Glu Thr Ile Ala Asn Leu Tyr Tyr Ala Asn Leu Thr Thr Val Asp Leu
115 120 125

Leu Lys Arg Phe Asn Ser Tyr Asp Pro Lys Asn Ile Pro Val Asn Ala
130 135 140

Lys Val Asn Val Thr Val Asn Cys Ser Cys Gly Asn Ser Gln Val Ser
145 150 155 160

Lys Asp Tyr Gly Leu Phe Ile Thr Tyr Pro Ile Arg Pro Gly Asp Thr
165 170 175

Leu Gln Asp Ile Ala Asn Gln Ser Ser Leu Asp Ala Gly Leu Ile Gln
180 185 190

Ser Phe Asn Pro Ser Val Asn Phe Ser Lys Asp Ser Gly Ile Ala Phe
195 200 205

Ile Pro Gly Arg Tyr Lys Asn Gly Val Tyr Val Pro Leu Tyr His Arg
210 215 220

Thr Ala Gly Leu Ala Ser Gly Ala Ala Val Gly Ile Ser Ile Ala Gly
225 230 235 240

Thr Phe Val Leu Leu Leu Leu Ala Phe Cys Met Tyr Val Arg Tyr Gln
245 250 255

Lys Lys Glu Glu Glu Lys Ala Lys Leu Pro Thr Asp Ile Ser Met Ala
260 265 270

Leu Ser Thr Gln Asp Ala Ser Ser Ser Ala Glu Tyr Glu Thr Ser Gly
275 280 285

Ser Ser Gly Pro Gly Thr Ala Ser Ala Thr Gly Leu Thr Ser Ile Met
290 295 300

Val Ala Lys Ser Met Glu Phe Ser Tyr Gln Glu Leu Ala Lys Ala Thr
305 310 315 320

Asn Asn Phe Ser Leu Asp Asn Lys Ile Gly Gln Gly Gly Phe Gly Ala
325 330 335

Val Tyr Tyr Ala Glu Leu Arg Gly Lys Lys Thr Ala Ile Lys Lys Met
340 345 350

Asp Val Gln Ala Ser Thr Glu Phe Leu Cys Glu Leu Lys Val Leu Thr
355 360 365

His Val His His Leu Asn Leu Val Arg Leu Ile Gly Tyr Cys Val Glu
370 375 380

Gly Ser Leu Phe Leu Val Tyr Glu His Ile Asp Asn Gly Asn Leu Gly
385 390 395 400

Gln Tyr Leu His Gly Ser Gly Lys Glu Pro Leu Pro Trp Ser Ser Arg
405 410 415

Val Gln Ile Ala Leu Asp Ala Ala Arg Gly Leu Glu Tyr Ile His Glu

420					425					430						
His	Thr	Val	Pro	Val	Tyr	Ile	His	Arg	Asp	Val	Lys	Ser	Ala	Asn	Ile	
435					440					445						
Leu	Ile	Asp	Lys	Asn	Leu	Arg	Gly	Lys	Val	Ala	Asp	Phe	Gly	Leu	Thr	
450					455					460						
Lys	Leu	Ile	Glu	Val	Gly	Asn	Ser	Thr	Leu	Gln	Thr	Arg	Leu	Val	Gly	
465					470					475					480	
Thr	Phe	Gly	Tyr	Met	Pro	Pro	Glu	Tyr	Ala	Gln	Tyr	Gly	Asp	Ile	Ser	
485					490					495						
Pro	Lys	Ile	Asp	Val	Tyr	Ala	Phe	Gly	Val	Val	Leu	Phe	Glu	Leu	Ile	
500					505					510						
Ser	Ala	Lys	Asn	Ala	Val	Leu	Lys	Thr	Gly	Glu	Leu	Val	Ala	Glu	Ser	
515					520					525						
Lys	Gly	Leu	Val	Ala	Leu	Phe	Glu	Glu	Ala	Leu	Asn	Lys	Ser	Asp	Pro	
530					535					540						
Cys	Asp	Ala	Leu	Arg	Lys	Leu	Val	Asp	Pro	Arg	Leu	Gly	Glu	Asn	Tyr	
545					550					555					560	
Pro	Ile	Asp	Ser	Val	Leu	Lys	Ile	Ala	Gln	Leu	Gly	Arg	Ala	Cys	Thr	
565					570					575						
Arg	Asp	Asn	Pro	Leu	Leu	Arg	Pro	Ser	Met	Arg	Ser	Leu	Val	Val	Ala	
580					585					590						
Leu	Met	Thr	Leu	Ser	Ser	Leu	Thr	Glu	Asp	Cys	Asp	Asp	Glu	Ser	Ser	
595					600					605						
Tyr	Glu	Ser	Gln	Thr	Leu	Ile	Asn	Leu	Leu	Ser	Val	Arg				
610					615					620						

<210> 25
 <211> 623
 <212> PRT
 <213> Lotus japonicus Gifu
 <400> 25

Met Lys Leu Lys Thr Gly Leu Leu Leu Phe Phe Ile Leu Leu Leu Gly
1 5 10 15

His Val Cys Phe His Val Glu Ser Asn Cys Leu Lys Gly Cys Asp Leu
20 25 30

Ala Leu Ala Ser Tyr Tyr Ile Leu Pro Gly Val Phe Ile Leu Gln Asn
35 40 45

Ile Thr Thr Phe Met Gln Ser Glu Ile Val Ser Ser Asn Asp Ala Ile
50 55 60

Thr Ser Tyr Asn Lys Asp Lys Ile Leu Asn Asp Ile Asn Ile Gln Ser
65 70 75 80

Phe Gln Arg Leu Asn Ile Pro Phe Pro Cys Asp Cys Ile Gly Gly Glu
85 90 95

Phe Leu Gly His Val Phe Glu Tyr Ser Ala Ser Lys Gly Asp Thr Tyr
100 105 110

Glu Thr Ile Ala Asn Leu Tyr Tyr Ala Asn Leu Thr Thr Val Asp Leu
115 120 125

Leu Lys Arg Phe Asn Ser Tyr Asp Pro Lys Asn Ile Pro Val Asn Ala
130 135 140

Lys Val Asn Val Thr Val Asn Cys Ser Cys Gly Asn Ser Gln Val Ser
145 150 155 160

Lys Asp Tyr Gly Leu Phe Ile Thr Tyr Pro Ile Arg Pro Gly Asp Thr
165 170 175

Leu Gln Asp Ile Ala Asn Gln Ser Ser Leu Asp Ala Gly Leu Ile Gln
180 185 190

Ser Phe Asn Pro Ser Val Asn Phe Ser Lys Asp Ser Gly Ile Ala Phe
195 200 205

Ile Pro Gly Arg Tyr Lys Asn Gly Val Tyr Val Pro Leu Tyr His Arg
210 215 220

Thr Ala Gly Leu Ala Ser Gly Ala Ala Val Gly Ile Ser Ile Ala Gly
225 230 235 240

Thr Phe Val Leu Leu Leu Leu Ala Phe Cys Met Tyr Val Arg Tyr Gln
245 250 255

Lys Lys Glu Glu Glu Lys Ala Lys Leu Pro Thr Asp Ile Ser Met Ala
260 265 270

Leu Ser Thr Gln Asp Ala Gly Asn Ser Ser Ser Ala Glu Tyr Glu Thr
275 280 285

Ser Gly Ser Ser Gly Pro Gly Thr Ala Ser Ala Thr Gly Leu Thr Ser
290 295 300

Ile Met Val Ala Lys Ser Met Glu Phe Ser Tyr Gln Glu Leu Ala Lys
305 310 315 320

Ala Thr Asn Asn Phe Ser Leu Asp Asn Lys Ile Gly Gln Gly Gly Phe
325 330 335

Gly Ala Val Tyr Tyr Ala Glu Leu Arg Gly Lys Lys Thr Ala Ile Lys
340 345 350

Lys Met Asp Val Gln Ala Ser Thr Glu Phe Leu Cys Glu Leu Lys Val
355 360 365

Leu Thr His Val His His Leu Asn Leu Val Arg Leu Ile Gly Tyr Cys
370 375 380

Val Glu Gly Ser Leu Phe Leu Val Tyr Glu His Ile Asp Asn Gly Asn
385 390 395 400

Leu Gly Gln Tyr Leu His Gly Ser Gly Lys Glu Pro Leu Pro Trp Ser
405 410 415

Ser Arg Val Gln Ile Ala Leu Asp Ala Ala Arg Gly Leu Glu Tyr Ile
420 425 430

His Glu His Thr Val Pro Val Tyr Ile His Arg Asp Val Lys Ser Ala
435 440 445

Asn Ile Leu Ile Asp Lys Asn Leu Arg Gly Lys Val Ala Asp Phe Gly

450	455	460
Leu Thr Lys Leu Ile Glu Val Gly Asn Ser Thr Leu Gln Thr Arg Leu 465	470	475 480
Val Gly Thr Phe Gly Tyr Met Pro Pro Glu Tyr Ala Gln Tyr Gly Asp 485	490	495
Ile Ser Pro Lys Ile Asp Val Tyr Ala Phe Gly Val Val Leu Phe Glu 500	505	510
Leu Ile Ser Ala Lys Asn Ala Val Leu Lys Thr Gly Glu Leu Val Ala 515	520	525
Glu Ser Lys Gly Leu Val Ala Leu Phe Glu Glu Ala Leu Asn Lys Ser 530	535	540
Asp Pro Cys Asp Ala Leu Arg Lys Leu Val Asp Pro Arg Leu Gly Glu 545	550	555 560
Asn Tyr Pro Ile Asp Ser Val Leu Lys Ile Ala Gln Leu Gly Arg Ala 565	570	575
Cys Thr Arg Asp Asn Pro Leu Leu Arg Pro Ser Met Arg Ser Leu Val 580	585	590
Val Ala Leu Met Thr Leu Ser Ser Leu Thr Glu Asp Cys Asp Asp Glu 595	600	605
Ser Ser Tyr Glu Ser Gln Thr Leu Ile Asn Leu Leu Ser Val Arg 610	615	620

<210> 26
 <211> 19
 <212> DNA
 <213> Lotus japonicus

<400> 26
 aatgctcttg atcaggctg
 19

<210> 27
 <211> 20
 <212> DNA
 <213> Lotus japonicus

<400> 27
aggagcccaa gtgagtgcta
20

<210> 28
<211> 20
<212> DNA
<213> Lotus japonicus

<400> 28
caggaaaaac caccacctgt
20

<210> 29
<211> 21
<212> DNA
<213> Lotus japonicus

<400> 29
atggaggcga atacactggt g
21

<210> 30
<211> 1853
<212> DNA
<213> Lotus filicaulis

<400> 30
ttttctcttt cctgtttaac tatcatttgt tcccaacttc acaaacatgg ctgtcttctt
60

tcttacctct ggcctctctga gtctttttct tgcactcacg ttgcttttca ctaacatcgc
120

cgctcgatca gaacagatca gcggcccaga cttttcatgc cctgttgact cacctccttc
180

ttgtgaaaca tatgtgacat acacagctca gtctccaaat cttctgagcc tgacaaacat
240

atctgatata ttgatatca gtcctttgtc cattgcaaga gccagtaaca tagatgcagg
300

gaaggacaag ctggttccag gccaaagtct actggtacct gtaacttgcg gttgcgcgg
360

aaaccactct tctgccaata cctcctacca aatccagaaa ggtgatagct acgactttgt
420

tgcaaccact ttatatgaga accttacaaa ttggaatata gtacaagctt caaaccagg
480

ggtaaatacca tatttggtgc cagagcgcgt caaagtcgta ttccctttat tctgcagggtg
540

cccttcaaag aaccagttga acaaagggat tcagtatctg attacttatg tgtggaagcc
600

caatgacaat gtttcccttg tgagtgccaa gtttggtgca tccccagcgg acatattgac
660

tgaaaaccgc tacgggtcaag acttcaactgc tgcaaccaac cttccaatth tgatcccagt
720

gacacagttg ccaaagctta ctcaaccttc ttcaaattga aggaaaagca gcattcatct
780

tctggttata cttggtatta ccctgggatg cacgttgcta actgcagttt taaccgggac
840

cctcgatatat gtatactgcc gcagaaagaa ggctctgaat aggactgctt catcagctga
900

gactgctgat aaactacttt ctggagtttc aggctatgta agcaagccaa acgtgtatga
960

aatcgacgag ataattggaag ctacgaagga tttcagcgtat gaggcgcaagg ttgggggaatc
1020

agtggtacaag gccaacatag aagggtcgggt tgtagcggta aagaaaatca aggaagggtgg
1080

tgccaatgag gaactgaaaa ttctgcagaa ggtaaatcat ggaaatctgg tgaaactaat
1140

gggtgtctcc tcaggctatg atggaaaactg tttcttggtt tatgaatatg ctgaaaatgg
1200

gtctcttgct gagggtgctg tctccaagtc ttcaggaacc ccaaactccc ttacatggtc
1260

tcaaaggata agcatagcag tggatgttgc tgtgggtctg caatacatgc atgaacatac
1320

ctatccaaga ataatacaca gggacatcac aacaagtaat atccttctcg actcgacctt
1380

caaggccaag atagcaaatt tcgccatggc cagaacttcg accaaccoca tgatgccaaa
1440

aatcgatgtc ttcgctttcg gggtgcttct gatagagttg ctcaccggaa ggaaagccat
1500

gacaaccaag gagaacggcg aggtgggttat gctgtggaag gatatgtggg agatctttga
1560

catagaagag aatagagagg agaggatcag aaaatggatg gatcctaatt tagagagctt
1620

ttatcatata gataatgctc tcagcttggc atccttagca gtgaattgca cagctgataa
1680

gtctttgtct cgaccctcca tggtgaaat tgttcttagc ctctcctttc tcaactcaaca
1740

atcatctaac cccacattag agagatcctt gacttcttct gggttagatg tagaagatga
1800

tgctcatatt gtcacttcca ttacagcacg ttaagcaagg gaaggtaatt cag
1853

<210> 31

<211> 595

<212> PRT

<213> Lotus filicaulis

<400> 31

Met Ala Val Phe Phe Leu Thr Ser Gly Ser Leu Ser Leu Phe Leu Ala
1 5 10 15

Leu Thr Leu Leu Phe Thr Asn Ile Ala Ala Arg Ser Glu Gln Ile Ser
20 25 30

Gly Pro Asp Phe Ser Cys Pro Val Asp Ser Pro Pro Ser Cys Glu Thr
35 40 45

Tyr Val Thr Tyr Thr Ala Gln Ser Pro Asn Leu Leu Ser Leu Thr Asn
50 55 60

Ile Ser Asp Ile Phe Asp Ile Ser Pro Leu Ser Ile Ala Arg Ala Ser
65 70 75 80

Asn Ile Asp Ala Gly Lys Asp Lys Leu Val Pro Gly Gln Val Leu Leu
85 90 95

Val Pro Val Thr Cys Gly Cys Ala Gly Asn His Ser Ser Ala Asn Thr
100 105 110

Ser Tyr Gln Ile Gln Lys Gly Asp Ser Tyr Asp Phe Val Ala Thr Thr
115 120 125

Leu Tyr Glu Asn Leu Thr Asn Trp Asn Ile Val Gln Ala Ser Asn Pro
130 135 140

Gly Val Asn Pro Tyr Leu Leu Pro Glu Arg Val Lys Val Val Phe Pro

145		150		155		160
Leu Phe Cys Arg Cys Pro Ser Lys Asn Gln Leu Asn Lys Gly Ile Gln						
	165		170		175	
Tyr Leu Ile Thr Tyr Val Trp Lys Pro Asn Asp Asn Val Ser Leu Val						
	180		185		190	
Ser Ala Lys Phe Gly Ala Ser Pro Ala Asp Ile Leu Thr Glu Asn Arg						
	195		200		205	
Tyr Gly Gln Asp Phe Thr Ala Ala Thr Asn Leu Pro Ile Leu Ile Pro						
	210		215		220	
Val Thr Gln Leu Pro Lys Leu Thr Gln Pro Ser Ser Asn Gly Arg Lys						
	225		230		235	240
Ser Ser Ile His Leu Leu Val Ile Leu Gly Ile Thr Leu Gly Cys Thr						
	245		250		255	
Leu Leu Thr Ala Val Leu Thr Gly Thr Leu Val Tyr Val Tyr Cys Arg						
	260		265		270	
Arg Lys Lys Ala Leu Asn Arg Thr Ala Ser Ser Ala Glu Thr Ala Asp						
	275		280		285	
Lys Leu Leu Ser Gly Val Ser Gly Tyr Val Ser Lys Pro Asn Val Tyr						
	290		295		300	
Glu Ile Asp Glu Ile Met Glu Ala Thr Lys Asp Phe Ser Asp Glu Cys						
	305		310		315	320
Lys Val Gly Glu Ser Val Tyr Lys Ala Asn Ile Glu Gly Arg Val Val						
	325		330		335	
Ala Val Lys Lys Ile Lys Glu Gly Gly Ala Asn Glu Glu Leu Lys Ile						
	340		345		350	
Leu Gln Lys Val Asn His Gly Asn Leu Val Lys Leu Met Gly Val Ser						
	355		360		365	
Ser Gly Tyr Asp Gly Asn Cys Phe Leu Val Tyr Glu Tyr Ala Glu Asn						
	370		375		380	

Gly Ser Leu Ala Glu Trp Leu Phe Ser Lys Ser Ser Gly Thr Pro Asn
385 390 395 400

Ser Leu Thr Trp Ser Gln Arg Ile Ser Ile Ala Val Asp Val Ala Val
405 410 415

Gly Leu Gln Tyr Met His Glu His Thr Tyr Pro Arg Ile Ile His Arg
420 425 430

Asp Ile Thr Thr Ser Asn Ile Leu Leu Asp Ser Thr Phe Lys Ala Lys
435 440 445

Ile Ala Asn Phe Ala Met Ala Arg Thr Ser Thr Asn Pro Met Met Pro
450 455 460

Lys Ile Asp Val Phe Ala Phe Gly Val Leu Leu Ile Glu Leu Leu Thr
465 470 475 480

Gly Arg Lys Ala Met Thr Thr Lys Glu Asn Gly Glu Val Val Met Leu
485 490 495

Trp Lys Asp Met Trp Glu Ile Phe Asp Ile Glu Glu Asn Arg Glu Glu
500 505 510

Arg Ile Arg Lys Trp Met Asp Pro Asn Leu Glu Ser Phe Tyr His Ile
515 520 525

Asp Asn Ala Leu Ser Leu Ala Ser Leu Ala Val Asn Cys Thr Ala Asp
530 535 540

Lys Ser Leu Ser Arg Pro Ser Met Ala Glu Ile Val Leu Ser Leu Ser
545 550 555 560

Phe Leu Thr Gln Gln Ser Ser Asn Pro Thr Leu Glu Arg Ser Leu Thr
565 570 575

Ser Ser Gly Leu Asp Val Glu Asp Asp Ala His Ile Val Thr Ser Ile
580 585 590

Thr Ala Arg
595

<210> 32
<211> 595
<212> PRT
<213> Medicago truncatula

<220>
<221> PEPTIDE
<222> (1)..(595)

<400> 32

Met Ser Ala Phe Phe Leu Pro Ser Ser Ser His Ala Leu Phe Leu Val
1 5 10 15

Leu Met Leu Phe Phe Leu Thr Asn Ile Ser Ala Gln Pro Leu Tyr Ile
20 25 30

Ser Glu Thr Asn Phe Thr Cys Pro Val Asp Ser Pro Pro Ser Cys Glu
35 40 45

Thr Tyr Val Ala Tyr Arg Ala Gln Ser Pro Asn Phe Leu Ser Leu Ser
50 55 60

Asn Ile Ser Asp Ile Phe Asn Leu Ser Pro Leu Arg Ile Ala Lys Ala
65 70 75 80

Ser Asn Ile Glu Ala Glu Asp Lys Lys Leu Ile Pro Asp Gln Leu Leu
85 90 95

Leu Val Pro Val Thr Cys Gly Cys Thr Lys Asn His Ser Phe Ala Asn
100 105 110

Ile Thr Tyr Ser Ile Lys Gln Gly Asp Asn Phe Phe Ile Leu Ser Ile
115 120 125

Thr Ser Tyr Gln Asn Leu Thr Asn Tyr Leu Glu Phe Lys Asn Phe Asn
130 135 140

Pro Asn Leu Ser Pro Thr Leu Leu Pro Leu Asp Thr Lys Val Ser Val
145 150 155 160

Pro Leu Phe Cys Lys Cys Pro Ser Lys Asn Gln Leu Asn Lys Gly Ile
165 170 175

Lys Tyr Leu Ile Thr Tyr Val Trp Gln Asp Asn Asp Asn Val Thr Leu
180 185 190

Val Ser Ser Lys Phe Gly Ala Ser Gln Val Glu Met Leu Ala Glu Asn
195 200 205

Asn His Asn Phe Thr Ala Ser Thr Asn Arg Ser Val Leu Ile Pro Val
210 215 220

Thr Ser Leu Pro Lys Leu Asp Gln Pro Ser Ser Asn Gly Arg Lys Ser
225 230 235 240

Ser Ser Gln Asn Leu Ala Leu Ile Ile Gly Ile Ser Leu Gly Ser Ala
245 250 255

Phe Phe Ile Leu Val Leu Thr Leu Ser Leu Val Tyr Val Tyr Cys Leu
260 265 270

Lys Met Lys Arg Leu Asn Arg Ser Thr Ser Ser Ser Glu Thr Ala Asp
275 280 285

Lys Leu Leu Ser Gly Val Ser Gly Tyr Val Ser Lys Pro Thr Met Tyr
290 295 300

Glu Ile Asp Ala Ile Met Glu Gly Thr Thr Asn Leu Ser Asp Asn Cys
305 310 315 320

Lys Ile Gly Glu Ser Val Tyr Lys Ala Asn Ile Asp Gly Arg Val Leu
325 330 335

Ala Val Lys Lys Ile Lys Lys Asp Ala Ser Glu Glu Leu Lys Ile Leu
340 345 350

Gln Lys Val Asn His Gly Asn Leu Val Lys Leu Met Gly Val Ser Ser
355 360 365

Asp Asn Asp Gly Asn Cys Phe Leu Val Tyr Glu Tyr Ala Glu Asn Gly
370 375 380

Ser Leu Glu Glu Trp Leu Phe Ser Glu Ser Ser Lys Thr Ser Asn Ser
385 390 395 400

Val Val Ser Leu Thr Trp Ser Gln Arg Ile Thr Ile Ala Met Asp Val

405	410	415
Ala Ile Gly Leu Gln Tyr Met His Glu His Thr Tyr Pro Arg Ile Ile 420 425 430		
His Arg Asp Ile Thr Thr Ser Asn Ile Leu Leu Gly Ser Asn Phe Lys 435 440 445		
Ala Lys Ile Ala Asn Phe Gly Met Ala Arg Thr Ser Thr Asn Ser Met 450 455 460		
Met Pro Lys Ile Asp Val Phe Ala Phe Gly Val Val Leu Ile Glu Leu 465 470 475 480		
Leu Thr Gly Lys Lys Ala Met Thr Thr Lys Glu Asn Gly Glu Val Val 485 490 495		
Ile Leu Trp Lys Asp Phe Trp Lys Ile Phe Asp Leu Glu Gly Asn Arg 500 505 510		
Glu Glu Arg Leu Arg Lys Trp Met Asp Pro Lys Leu Glu Ser Phe Tyr 515 520 525		
Pro Ile Asp Asn Ala Leu Ser Leu Ala Ser Leu Ala Val Asn Cys Thr 530 535 540		
Ala Asp Lys Ser Leu Ser Arg Pro Thr Ile Ala Glu Ile Val Leu Cys 545 550 555 560		
Leu Ser Leu Leu Asn Gln Pro Ser Ser Glu Pro Met Leu Glu Arg Ser 565 570 575		
Leu Thr Ser Gly Leu Asp Ala Glu Ala Thr His Val Val Thr Ser Val 580 585 590		
Ile Ala Arg 595		

<210> 33
 <211> 24
 <212> DNA
 <213> Phaseolus vulgaris

<220>
<221> misc_feature
<222> (1)..(24)
<223> Primer to amplify fragment of NPR5

<400> 33
cattgcaara gccagtaaca taga
24

<210> 34
<211> 30
<212> DNA
<213> Phaseolus vulgaris

<220>
<221> misc_feature
<222> (1)..(30)
<223> To amplify a fragment of NPR5

<400> 34
aacgwgwry wayrgaagtm acaayatgag
30

<210> 35
<211> 35
<212> DNA
<213> Phaseolus vulgaris

<220>
<221> misc_feature
<222> (1)..(35)
<223> NPR5 5'RACE primer

<400> 35
cgactgggat atgtatgtca catatgtttc acatg
35

<210> 36
<211> 22
<212> DNA
<213> Phaseolus vulgaris

<220>
<221> misc_feature
<222> (1)..(22)
<223> NPR5 3' RACE primer

<400> 36
gatagaattg cttactggca gg
22

<210> 37
<211> 21
<212> DNA
<213> Phaseolus vulgaris

<220>
<221> misc_feature
<222> (1)..(21)
<223> NPR5 gene PCR primer

<400> 37
gacgtgtcca ctgtatccag g
21

<210> 38
<211> 24
<212> DNA
<213> Phaseolus vulgaris

<220>
<221> misc_feature
<222> (1)..(24)
<223> NPR5 gene PCR primer

<400> 38
gttttgacat gcaataaaca actc
24

<210> 39
<211> 2164
<212> DNA
<213> Phaseolus vulgaris

<220>
<221> 5'UTR
<222> (1)..(172)

<220>
<221> CDS
<222> (173)..(1963)

<220>
<221> 3'UTR
<222> (1964)..(2164)

<400> 39
ggattcggaa agccaaaagg aaatttagtt aaagctaattg acacaaacag gaccatattt
60

ttatatattaag ccaaaagata tttttattga caaagaacta catatcaaca acgacgattg
120

ccagtgatag tagactgcct cataactttc atttggtcac aacttcacat ca atg gct
178

Met Ala
1

gtc ttc ttt gtt tct ctt act ctt ggt gct cag att ctt tat gtg gta
226

Val Phe Phe Val Ser Leu Thr Leu Gly Ala Gln Ile Leu Tyr Val Val
5 10 15

ctc atg ttt ttc act tgt att gaa gct caa tca caa cag acc aat gga
274

Leu Met Phe Phe Thr Cys Ile Glu Ala Gln Ser Gln Gln Thr Asn Gly
20 25 30

aca aac ttt tca tgc cct tcc aat tca cct cct tca tgt gaa aca tat
322

Thr Asn Phe Ser Cys Pro Ser Asn Ser Pro Pro Ser Cys Glu Thr Tyr
35 40 45 50

gtg aca tac ata tcc cag tcg cca aat ttt ttg agt ctg acc agc gta
370

Val Thr Tyr Ile Ser Gln Ser Pro Asn Phe Leu Ser Leu Thr Ser Val
55 60 65

tct aat ata ttt gac acg agt cct ttg tca att gcc aga gcc agc aac
418

Ser Asn Ile Phe Asp Thr Ser Pro Leu Ser Ile Ala Arg Ala Ser Asn
70 75 80

tta cag cat gag gaa gac aag ttg att cca ggc caa gtc tta ctg ata
466

Leu Gln His Glu Glu Asp Lys Leu Ile Pro Gly Gln Val Leu Leu Ile
85 90 95

cca gta acc tgt ggt tgc act gga aac cgc tct ttc gcc aac atc tcc
514

Pro Val Thr Cys Gly Cys Thr Gly Asn Arg Ser Phe Ala Asn Ile Ser
100 105 110

tat gag atc aac caa ggt gat agc ttc tac ttt gtt gcg acc act tta
562

Tyr Glu Ile Asn Gln Gly Asp Ser Phe Tyr Phe Val Ala Thr Thr Leu
115 120 125 130

tac cag aat ctc aca aat tgg cat gca gtg atg gat tta aac cca ggt
610

Tyr Gln Asn Leu Thr Asn Trp His Ala Val Met Asp Leu Asn Pro Gly
135 140 145

cta agt caa ttt act ttg cca ata ggc atc caa gtt gta att cct tta
658

Leu Ser Gln Phe Thr Leu Pro Ile Gly Ile Gln Val Val Ile Pro Leu
150 155 160

ttc tgc aag tgt cct tca aag aac cag ctg gat aga ggg ata aag tac
706
Phe Cys Lys Cys Pro Ser Lys Asn Gln Leu Asp Arg Gly Ile Lys Tyr
165 170 175

ctg atc act cac gtc tgg cag ccc aat gac aat gtt tcc ttt gta agt
754
Leu Ile Thr His Val Trp Gln Pro Asn Asp Asn Val Ser Phe Val Ser
180 185 190

aac aag tta ggt gca tca cca cag gac ata ttg agt gaa aac aac tat
802
Asn Lys Leu Gly Ala Ser Pro Gln Asp Ile Leu Ser Glu Asn Asn Tyr
195 200 205 210

ggt caa aat ttc act gcc gca agc aac ctt cca gtt ttg atc cca gtt
850
Gly Gln Asn Phe Thr Ala Ala Ser Asn Leu Pro Val Leu Ile Pro Val
215 220 225

aca ctc ttg cca gat ctt att caa tct cct tca gat gga aga aaa cac
898
Thr Leu Leu Pro Asp Leu Ile Gln Ser Pro Ser Asp Gly Arg Lys His
230 235 240

aga att ggt ctt cca gtt ata att ggt atc agc ctg gga tgc aca cta
946
Arg Ile Gly Leu Pro Val Ile Ile Gly Ile Ser Leu Gly Cys Thr Leu
245 250 255

ctg gtt gtg gtt tca gca ata tta ctg gtg tgt gta tgt tgt ctg aaa
994
Leu Val Val Val Ser Ala Ile Leu Leu Val Cys Val Cys Cys Leu Lys
260 265 270

atg aag agt ttg aat agg agt gct tca tca gct gaa act gca gat aaa
1042
Met Lys Ser Leu Asn Arg Ser Ala Ser Ser Ala Glu Thr Ala Asp Lys
275 280 285 290

cta ctt tct gga gtt tca ggc tat gta agt aag cct aca atg tat gaa
1090
Leu Leu Ser Gly Val Ser Gly Tyr Val Ser Lys Pro Thr Met Tyr Glu
295 300 305

act ggt gca ata ttg gaa gct act atg aac ctc agt gag cag tgc aag
1138
Thr Gly Ala Ile Leu Glu Ala Thr Met Asn Leu Ser Glu Gln Cys Lys
310 315 320

att ggg gaa tca gtg tac aag gct aac ata gag ggt aag gtt tta gca
1186
Ile Gly Glu Ser Val Tyr Lys Ala Asn Ile Glu Gly Lys Val Leu Ala
325 330 335

gta aaa aga ttc aag gaa gat gtc acg gag gag ctg aaa att ctg cag
1234

Val Lys Arg Phe Lys Glu Asp Val Thr Glu Glu Leu Lys Ile Leu Gln
 340 345 350
 aag gtg aat cat gga aat ctg gtg aaa cta atg ggt gtc tca tca gat
 1282
 Lys Val Asn His Gly Asn Leu Val Lys Leu Met Gly Val Ser Ser Asp
 355 360 365 370
 aat gat gga aat tgt ttt gtg gtt tat gaa tat gct gaa aat ggg tct
 1330
 Asn Asp Gly Asn Cys Phe Val Val Tyr Glu Tyr Ala Glu Asn Gly Ser
 375 380 385
 ctt gaa gag tgg ctt ttc gcc aag tct tgt tca gag aca tca aac tca
 1378
 Leu Glu Glu Trp Leu Phe Ala Lys Ser Cys Ser Glu Thr Ser Asn Ser
 390 395 400
 agg acc tcc ctt aca tgg tgc cag agg ata agc ata gca gtg gat gtt
 1426
 Arg Thr Ser Leu Thr Trp Cys Gln Arg Ile Ser Ile Ala Val Asp Val
 405 410 415
 tca atg ggt ctg cag tac atg cat gaa cat gct tat cca aga ata gtc
 1474
 Ser Met Gly Leu Gln Tyr Met His Glu His Ala Tyr Pro Arg Ile Val
 420 425 430
 cac agg gac atc aca agc agt aat atc ctt ctt gac tcc aac ttt aag
 1522
 His Arg Asp Ile Thr Ser Ser Asn Ile Leu Leu Asp Ser Asn Phe Lys
 435 440 445 450
 gcc aag ata gca aat ttc tcc atg gcc aga act ttt acc aac ccc atg
 1570
 Ala Lys Ile Ala Asn Phe Ser Met Ala Arg Thr Phe Thr Asn Pro Met
 455 460 465
 atg tca aaa ata gat gta ttt gct ttt ggg gtg gtt ctg ata gaa ttg
 1618
 Met Ser Lys Ile Asp Val Phe Ala Phe Gly Val Val Leu Ile Glu Leu
 470 475 480
 ctt act ggc agg aaa gcc atg aca acc aaa gaa aat ggt gag gtg gtt
 1666
 Leu Thr Gly Arg Lys Ala Met Thr Thr Lys Glu Asn Gly Glu Val Val
 485 490 495
 atg ctg tgg aag gac att tgg aag atc ttt gat caa gaa gag aat aga
 1714
 Met Leu Trp Lys Asp Ile Trp Lys Ile Phe Asp Gln Glu Glu Asn Arg
 500 505 510
 gag gag agg ctc aga aaa tgg atg gat cct aag tta gat aat tat tat
 1762
 Glu Glu Arg Leu Arg Lys Trp Met Asp Pro Lys Leu Asp Asn Tyr Tyr
 515 520 525 530

cct att gat tat gct ctc agc ttg gcc tcc ttg gca gtg aat tgc act
1810

Pro Ile Asp Tyr Ala Leu Ser Leu Ala Ser Leu Ala Val Asn Cys Thr
535 540 545

gca gac aag tct ttg tcc aga cca acc ata gca gaa att gtc ctt agt
1858

Ala Asp Lys Ser Leu Ser Arg Pro Thr Ile Ala Glu Ile Val Leu Ser
550 555 560

ctc tcc ctt ctc act caa cca tct ccc gcg aca ctg gag aga tcc ttg
1906

Leu Ser Leu Leu Thr Gln Pro Ser Pro Ala Thr Leu Glu Arg Ser Leu
565 570 575

act tct tct gga tta gat gta gaa gct act caa att gtc act tcc atc
1954

Thr Ser Ser Gly Leu Asp Val Glu Ala Thr Gln Ile Val Thr Ser Ile
580 585 590

tca gct cgt tgattgagtg aagccaatct agtttctcac atccaagatg
2003

Ser Ala Arg
595

gtactttttt ttaaataatg attgcacctt agtcaataat gatgaacttg gtttatgggg
2063

agttttcaac atttagtggt tccatccctg ttgttcttta tgtttgaggt agagttcgta
2123

aaacgaatag caattgcagt tctcctcaga ctaaatttgc t
2164

<210> 40

<211> 597

<212> PRT

<213> Phaseolus vulgaris

<400> 40

Met Ala Val Phe Phe Val Ser Leu Thr Leu Gly Ala Gln Ile Leu Tyr
1 5 10 15

Val Val Leu Met Phe Phe Thr Cys Ile Glu Ala Gln Ser Gln Gln Thr
20 25 30

Asn Gly Thr Asn Phe Ser Cys Pro Ser Asn Ser Pro Pro Ser Cys Glu
35 40 45

Thr Tyr Val Thr Tyr Ile Ser Gln Ser Pro Asn Phe Leu Ser Leu Thr
50 55 60

Ser Val Ser Asn Ile Phe Asp Thr Ser Pro Leu Ser Ile Ala Arg Ala
65 70 75 80

Ser Asn Leu Gln His Glu Glu Asp Lys Leu Ile Pro Gly Gln Val Leu
85 90 95

Leu Ile Pro Val Thr Cys Gly Cys Thr Gly Asn Arg Ser Phe Ala Asn
100 105 110

Ile Ser Tyr Glu Ile Asn Gln Gly Asp Ser Phe Tyr Phe Val Ala Thr
115 120 125

Thr Leu Tyr Gln Asn Leu Thr Asn Trp His Ala Val Met Asp Leu Asn
130 135 140

Pro Gly Leu Ser Gln Phe Thr Leu Pro Ile Gly Ile Gln Val Val Ile
145 150 155 160

Pro Leu Phe Cys Lys Cys Pro Ser Lys Asn Gln Leu Asp Arg Gly Ile
165 170 175

Lys Tyr Leu Ile Thr His Val Trp Gln Pro Asn Asp Asn Val Ser Phe
180 185 190

Val Ser Asn Lys Leu Gly Ala Ser Pro Gln Asp Ile Leu Ser Glu Asn
195 200 205

Asn Tyr Gly Gln Asn Phe Thr Ala Ala Ser Asn Leu Pro Val Leu Ile
210 215 220

Pro Val Thr Leu Leu Pro Asp Leu Ile Gln Ser Pro Ser Asp Gly Arg
225 230 235 240

Lys His Arg Ile Gly Leu Pro Val Ile Ile Gly Ile Ser Leu Gly Cys
245 250 255

Thr Leu Leu Val Val Val Ser Ala Ile Leu Leu Val Cys Val Cys Cys
260 265 270

Leu Lys Met Lys Ser Leu Asn Arg Ser Ala Ser Ser Ala Glu Thr Ala
275 280 285

Asp Lys Leu Leu Ser Gly Val Ser Gly Tyr Val Ser Lys Pro Thr Met
290 295 300

Tyr Glu Thr Gly Ala Ile Leu Glu Ala Thr Met Asn Leu Ser Glu Gln
305 310 315 320

Cys Lys Ile Gly Glu Ser Val Tyr Lys Ala Asn Ile Glu Gly Lys Val
325 330 335

Leu Ala Val Lys Arg Phe Lys Glu Asp Val Thr Glu Glu Leu Lys Ile
340 345 350

Leu Gln Lys Val Asn His Gly Asn Leu Val Lys Leu Met Gly Val Ser
355 360 365

Ser Asp Asn Asp Gly Asn Cys Phe Val Val Tyr Glu Tyr Ala Glu Asn
370 375 380

Gly Ser Leu Glu Glu Trp Leu Phe Ala Lys Ser Cys Ser Glu Thr Ser
385 390 395 400

Asn Ser Arg Thr Ser Leu Thr Trp Cys Gln Arg Ile Ser Ile Ala Val
405 410 415

Asp Val Ser Met Gly Leu Gln Tyr Met His Glu His Ala Tyr Pro Arg
420 425 430

Ile Val His Arg Asp Ile Thr Ser Ser Asn Ile Leu Leu Asp Ser Asn
435 440 445

Phe Lys Ala Lys Ile Ala Asn Phe Ser Met Ala Arg Thr Phe Thr Asn
450 455 460

Pro Met Met Ser Lys Ile Asp Val Phe Ala Phe Gly Val Val Leu Ile
465 470 475 480

Glu Leu Leu Thr Gly Arg Lys Ala Met Thr Thr Lys Glu Asn Gly Glu
485 490 495

Val Val Met Leu Trp Lys Asp Ile Trp Lys Ile Phe Asp Gln Glu Glu
500 505 510

Asn Arg Glu Glu Arg Leu Arg Lys Trp Met Asp Pro Lys Leu Asp Asn
515 520 525

Tyr Tyr Pro Ile Asp Tyr Ala Leu Ser Leu Ala Ser Leu Ala Val Asn
530 535 540

Cys Thr Ala Asp Lys Ser Leu Ser Arg Pro Thr Ile Ala Glu Ile Val
545 550 555 560

Leu Ser Leu Ser Leu Leu Thr Gln Pro Ser Pro Ala Thr Leu Glu Arg
565 570 575

Ser Leu Thr Ser Ser Gly Leu Asp Val Glu Ala Thr Gln Ile Val Thr
580 585 590

Ser Ile Ser Ala Arg
595

<210> 41
<211> 24
<212> DNA
<213> Glycine max

<220>
<221> misc_feature
<222> (1)..(24)
<223> Primer to amplify NPR5 gene fragment

<400> 41
cattgcaara gccagtaaca taga
24

<210> 42
<211> 30
<212> DNA
<213> Glycine max

<220>
<221> misc_feature
<222> (1)..(30)
<223> Primer to amplify NPR5 gene fragment

<400> 42
aacgwgwry wayrgaagtm acaayatgag
30

<210> 43

<211> 31
<212> DNA
<213> Glycine max

<220>
<221> misc_feature
<222> (1)..(31)
<223> NPR5 5'RACE primer

<400> 43
ccatcactgc acgccaattc gtgagattct c
31

<210> 44
<211> 19
<212> DNA
<213> Glycine max

<220>
<221> misc_feature
<222> (1)..(19)
<223> NPR5 3'RACE primer

<400> 44
gatgtctttg catttgagg
19

<210> 45
<211> 26
<212> DNA
<213> Glycine max

<220>
<221> misc_feature
<222> (1)..(27)
<223> NPR5 gene PCR primers

<400> 45
ctaatacgac ataccaacaa ctgcag
26

<210> 46
<211> 24
<212> DNA
<213> Glycine max

<220>
<221> misc_feature
<222> (1)..(24)
<223> NPR5 gene PCR primer

<400> 46
ctcgcttgaa tttgtttgta catg
24

<210> 47
<211> 2130
<212> DNA
<213> Glycine max

<220>
<221> 5'UTR
<222> (1)..(68)

<220>
<221> CDS
<222> (69)..(1862)

<220>
<221> 3'UTR
<222> (1863)..(2130)

<400> 47
ttgcctgtga taatagactc tccttattct ttccctcggt acttacattt gttcacaact
60

aaacagca atg gct gtc ttc ttt ccc ttt ctt cct ctc cac tct cag att
110
Met Ala Val Phe Phe Pro Phe Leu Pro Leu His Ser Gln Ile
1 5 10

ctt tgt ctt gtg atc atg ttg ttt tcc act aat att gta gct caa tca
158
Leu Cys Leu Val Ile Met Leu Phe Ser Thr Asn Ile Val Ala Gln Ser
15 20 25 30

caa cag gac aat aga aca aac ttt tca tgc cct tct gat tca ccg cct
206
Gln Gln Asp Asn Arg Thr Asn Phe Ser Cys Pro Ser Asp Ser Pro Pro
35 40 45

tca tgt gaa acc tat gta aca tac att gct cag tct cca aat ttt ttg
254
Ser Cys Glu Thr Tyr Val Thr Tyr Ile Ala Gln Ser Pro Asn Phe Leu
50 55 60

agt cta acc aac ata tcc aat ata ttt gac aca agc cct tta tcc att
302
Ser Leu Thr Asn Ile Ser Asn Ile Phe Asp Thr Ser Pro Leu Ser Ile
65 70 75

gca aga gcc agt aac tta gag cct atg gat gac aag cta gtc aaa gac
350
Ala Arg Ala Ser Asn Leu Glu Pro Met Asp Asp Lys Leu Val Lys Asp
80 85 90

caa gtc tta ctc gta cca gta acc tgt ggt tgc act gga aac cgc tct
 398
 Gln Val Leu Leu Val Pro Val Thr Cys Gly Cys Thr Gly Asn Arg Ser
 95 100 105 110

ttt gcc aat atc tcc tat gag atc aac caa ggt gat agc ttc tac ttt
 446
 Phe Ala Asn Ile Ser Tyr Glu Ile Asn Gln Gly Asp Ser Phe Tyr Phe
 115 120 125

gtt gca acc act tca tac gag aat ctc acg aat tgg cgt gca gtg atg
 494
 Val Ala Thr Thr Ser Tyr Glu Asn Leu Thr Asn Trp Arg Ala Val Met
 130 135 140

gat tta aac ccc gtt cta agt cca aat aag ttg cca ata gga atc caa
 542
 Asp Leu Asn Pro Val Leu Ser Pro Asn Lys Leu Pro Ile Gly Ile Gln
 145 150 155

gta gta ttt cct tta ttc tgc aag tgc cct tca aag aac cag ttg gac
 590
 Val Val Phe Pro Leu Phe Cys Lys Cys Pro Ser Lys Asn Gln Leu Asp
 160 165 170

aaa gag ata aag tac ctg att aca tac gtg tgg aag ccc ggt gac aat
 638
 Lys Glu Ile Lys Tyr Leu Ile Thr Tyr Val Trp Lys Pro Gly Asp Asn
 175 180 185 190

gtt tcc ctt gta agt gac aag ttt ggt gca tca cca gag gac ata atg
 686
 Val Ser Leu Val Ser Asp Lys Phe Gly Ala Ser Pro Glu Asp Ile Met
 195 200 205

agt gaa aac aac tat ggt cag aac ttt act gct gca aac aac ctt cca
 734
 Ser Glu Asn Asn Tyr Gly Gln Asn Phe Thr Ala Ala Asn Asn Leu Pro
 210 215 220

gtt ctg atc cca gtg aca cgc ttg cca gtt ctt gct cga tct cct tcg
 782
 Val Leu Ile Pro Val Thr Arg Leu Pro Val Leu Ala Arg Ser Pro Ser
 225 230 235

gac gga aga aaa ggc gga att cgt ctt ccg gtt ata att ggt att agc
 830
 Asp Gly Arg Lys Gly Gly Ile Arg Leu Pro Val Ile Ile Gly Ile Ser
 240 245 250

ttg gga tgc acg cta ctg gtt ctg gtt tta gca gtg tta ctg gtg tat
 878
 Leu Gly Cys Thr Leu Leu Val Leu Val Leu Ala Val Leu Leu Val Tyr
 255 260 265 270

gta tat tgt ctg aaa atg aag act ttg aat agg agt gct tca tcg gct
 926
 Val Tyr Cys Leu Lys Met Lys Thr Leu Asn Arg Ser Ala Ser Ser Ala
 275 280 285

gaa act gca gat aaa cta ctt tct gga gtt tca ggc tat gta agt aag
 974
 Glu Thr Ala Asp Lys Leu Leu Ser Gly Val Ser Gly Tyr Val Ser Lys
 290 295 300

cct acc atg tat gaa act gat gcg atc atg gaa gct aca atg aac ctc
 1022
 Pro Thr Met Tyr Glu Thr Asp Ala Ile Met Glu Ala Thr Met Asn Leu
 305 310 315

agt gag cag tgc aag att ggg gaa tca gtg tac aag gca aac ata gag
 1070
 Ser Glu Gln Cys Lys Ile Gly Glu Ser Val Tyr Lys Ala Asn Ile Glu
 320 325 330

ggt aag gtt ttg gca gta aaa aga ttc aag gaa gat gtc acg gaa gag
 1118
 Gly Lys Val Leu Ala Val Lys Arg Phe Lys Glu Asp Val Thr Glu Glu
 335 340 345 350

ctg aaa att ctg cag aag gtg aat cat ggg aat ctg gtg aaa cta atg
 1166
 Leu Lys Ile Leu Gln Lys Val Asn His Gly Asn Leu Val Lys Leu Met
 355 360 365

ggt gtc tca tca gac aat gat gga aac tgt ttt gtg gtt tat gaa tac
 1214
 Gly Val Ser Ser Asp Asn Asp Gly Asn Cys Phe Val Val Tyr Glu Tyr
 370 375 380

gct gaa aat ggg tct ctt gat gag tgg cta ttc tcc aag tct tgt tca
 1262
 Ala Glu Asn Gly Ser Leu Asp Glu Trp Leu Phe Ser Lys Ser Cys Ser
 385 390 395

gac aca tca aac tca agg gca tcc ctt aca tgg tgt cag agg ata agc
 1310
 Asp Thr Ser Asn Ser Arg Ala Ser Leu Thr Trp Cys Gln Arg Ile Ser
 400 405 410

atg gca gtg gat gtt gcg atg ggt ttg cag tac atg cat gaa cat gct
 1358
 Met Ala Val Asp Val Ala Met Gly Leu Gln Tyr Met His Glu His Ala
 415 420 425 430

tat cca aga ata gtc cac agg gac atc aca agc agt aat atc ctt ctt
 1406
 Tyr Pro Arg Ile Val His Arg Asp Ile Thr Ser Ser Asn Ile Leu Leu
 435 440 445

gac tcg aac ttt aag gcc aag ata gca aat ttc tcc atg gcc aga act
 1454

Asp Ser Asn Phe Lys Ala Lys Ile Ala Asn Phe Ser Met Ala Arg Thr
450 455 460

ttt acc aac ccc atg atg cca aag ata gat gtc ttt gca ttt ggg gtg
1502

Phe Thr Asn Pro Met Met Pro Lys Ile Asp Val Phe Ala Phe Gly Val
465 470 475

gtt ctg att gag ttg ctt acc gga agg aaa gcc atg aca acc aag gaa
1550

Val Leu Ile Glu Leu Leu Thr Gly Arg Lys Ala Met Thr Thr Lys Glu
480 485 490

aat ggt gag gtg gtc atg ctg tgg aag gac att tgg aag atc ttt gat
1598

Asn Gly Glu Val Val Met Leu Trp Lys Asp Ile Trp Lys Ile Phe Asp
495 500 505 510

caa gaa gag aat aga gag gag agg ctc aaa aaa tgg atg gat cct aag
1646

Gln Glu Glu Asn Arg Glu Glu Arg Leu Lys Lys Trp Met Asp Pro Lys
515 520 525

tta gag agt tat tat cct ata gat tac gct ctc agc ttg gcc tcc ttg
1694

Leu Glu Ser Tyr Tyr Pro Ile Asp Tyr Ala Leu Ser Leu Ala Ser Leu
530 535 540

gcg gtg aat tgt act gca gat aag tct ttg tcc aga cca acc att gca
1742

Ala Val Asn Cys Thr Ala Asp Lys Ser Leu Ser Arg Pro Thr Ile Ala
545 550 555

gaa att gtc ctt agc ctc tcc ctt ctc act caa cca tct ccc gca aca
1790

Glu Ile Val Leu Ser Leu Ser Leu Leu Thr Gln Pro Ser Pro Ala Thr
560 565 570

ttg gag aga tcc ttg act tct tct gga ttg gat gta gaa gct act caa
1838

Leu Glu Arg Ser Leu Thr Ser Ser Gly Leu Asp Val Glu Ala Thr Gln
575 580 585 590

att gtc act tcc ata gca gct cgt tgattgagtg aaggaaattt agtttctcaa
1892

Ile Val Thr Ser Ile Ala Ala Arg
595

atccatgatg gtattttgtt tacatgatga ttattacatc tttagtcatt aatggttggc
1952

ttgggttggg ggagtgtgtt caaaatttcg tttttttcca tccctgttat tttttttaag
2012

tttggggtag agtcagcaaa aatggaagtt gcaattgacc tcagactaaa cttgcttatt
2072

tcacctgtatc ttttttgtgt gataattgaa actgaattat atgatggatt atctgtta
2130

<210> 48
<211> 598
<212> PRT
<213> Glycine max

<400> 48

Met Ala Val Phe Phe Pro Phe Leu Pro Leu His Ser Gln Ile Leu Cys
1 5 10 15

Leu Val Ile Met Leu Phe Ser Thr Asn Ile Val Ala Gln Ser Gln Gln
20 25 30

Asp Asn Arg Thr Asn Phe Ser Cys Pro Ser Asp Ser Pro Pro Ser Cys
35 40 45

Glu Thr Tyr Val Thr Tyr Ile Ala Gln Ser Pro Asn Phe Leu Ser Leu
50 55 60

Thr Asn Ile Ser Asn Ile Phe Asp Thr Ser Pro Leu Ser Ile Ala Arg
65 70 75 80

Ala Ser Asn Leu Glu Pro Met Asp Asp Lys Leu Val Lys Asp Gln Val
85 90 95

Leu Leu Val Pro Val Thr Cys Gly Cys Thr Gly Asn Arg Ser Phe Ala
100 105 110

Asn Ile Ser Tyr Glu Ile Asn Gln Gly Asp Ser Phe Tyr Phe Val Ala
115 120 125

Thr Thr Ser Tyr Glu Asn Leu Thr Asn Trp Arg Ala Val Met Asp Leu
130 135 140

Asn Pro Val Leu Ser Pro Asn Lys Leu Pro Ile Gly Ile Gln Val Val
145 150 155 160

Phe Pro Leu Phe Cys Lys Cys Pro Ser Lys Asn Gln Leu Asp Lys Glu
165 170 175

Ile Lys Tyr Leu Ile Thr Tyr Val Trp Lys Pro Gly Asp Asn Val Ser
180 185 190

Leu Val Ser Asp Lys Phe Gly Ala Ser Pro Glu Asp Ile Met Ser Glu
195 200 205

Asn Asn Tyr Gly Gln Asn Phe Thr Ala Ala Asn Asn Leu Pro Val Leu
210 215 220

Ile Pro Val Thr Arg Leu Pro Val Leu Ala Arg Ser Pro Ser Asp Gly
225 230 235 240

Arg Lys Gly Gly Ile Arg Leu Pro Val Ile Ile Gly Ile Ser Leu Gly
245 250 255

Cys Thr Leu Leu Val Leu Val Leu Ala Val Leu Leu Val Tyr Val Tyr
260 265 270

Cys Leu Lys Met Lys Thr Leu Asn Arg Ser Ala Ser Ser Ala Glu Thr
275 280 285

Ala Asp Lys Leu Leu Ser Gly Val Ser Gly Tyr Val Ser Lys Pro Thr
290 295 300

Met Tyr Glu Thr Asp Ala Ile Met Glu Ala Thr Met Asn Leu Ser Glu
305 310 315 320

Gln Cys Lys Ile Gly Glu Ser Val Tyr Lys Ala Asn Ile Glu Gly Lys
325 330 335

Val Leu Ala Val Lys Arg Phe Lys Glu Asp Val Thr Glu Glu Leu Lys
340 345 350

Ile Leu Gln Lys Val Asn His Gly Asn Leu Val Lys Leu Met Gly Val
355 360 365

Ser Ser Asp Asn Asp Gly Asn Cys Phe Val Val Tyr Glu Tyr Ala Glu
370 375 380

Asn Gly Ser Leu Asp Glu Trp Leu Phe Ser Lys Ser Cys Ser Asp Thr
385 390 395 400

Ser Asn Ser Arg Ala Ser Leu Thr Trp Cys Gln Arg Ile Ser Met Ala
405 410 415

Val Asp Val Ala Met Gly Leu Gln Tyr Met His Glu His Ala Tyr Pro
420 425 430

Arg Ile Val His Arg Asp Ile Thr Ser Ser Asn Ile Leu Leu Asp Ser
435 440 445

Asn Phe Lys Ala Lys Ile Ala Asn Phe Ser Met Ala Arg Thr Phe Thr
450 455 460

Asn Pro Met Met Pro Lys Ile Asp Val Phe Ala Phe Gly Val Val Leu
465 470 475 480

Ile Glu Leu Leu Thr Gly Arg Lys Ala Met Thr Thr Lys Glu Asn Gly
485 490 495

Glu Val Val Met Leu Trp Lys Asp Ile Trp Lys Ile Phe Asp Gln Glu
500 505 510

Glu Asn Arg Glu Glu Arg Leu Lys Lys Trp Met Asp Pro Lys Leu Glu
515 520 525

Ser Tyr Tyr Pro Ile Asp Tyr Ala Leu Ser Leu Ala Ser Leu Ala Val
530 535 540

Asn Cys Thr Ala Asp Lys Ser Leu Ser Arg Pro Thr Ile Ala Glu Ile
545 550 555 560

Val Leu Ser Leu Ser Leu Leu Thr Gln Pro Ser Pro Ala Thr Leu Glu
565 570 575

Arg Ser Leu Thr Ser Ser Gly Leu Asp Val Glu Ala Thr Gln Ile Val
580 585 590

Thr Ser Ile Ala Ala Arg
595

<210> 49
<211> 22
<212> DNA
<213> Lotus japonicus

<220>
<221> misc_feature

<222> (1)..(22)
<223> NPR5 extracellular domain coding sequence amplification primer

<400> 49
taattatcag agtaagtgtg ac
22

<210> 50
<211> 19
<212> DNA
<213> Lotus japonicus

<220>
<221> misc_feature
<222> (1)..(19)
<223> NPR5 extracellular domain coding sequence amplification primer

<400> 50
agttaccac ctgtggtac
19

<210> 51
<211> 2160
<212> DNA
<213> Pisum sativum

<220>
<221> 5'UTR
<222> (1)..(65)

<220>
<221> CDS
<222> (66)..(1931)

<220>
<221> 3'UTR
<222> (1932)..(2160)

<400> 51
ttttttctgc ttcttccttt tcttcaggag ccattttgat ttgctctctt tcttattgac
60

caaat atg aaa cta aaa aat ggc tta ctc ttg ttc ttt cta ttt gtg gag
110

Met	Lys	Leu	Lys	Asn	Gly	Leu	Leu	Leu	Phe	Phe	Leu	Phe	Val	Glu
1				5					10				15	

tgt gct ttt ttc aaa gtg gat tca aag tgt gtg aaa ggg tgt gat cta
158

Cys	Ala	Phe	Phe	Lys	Val	Asp	Ser	Lys	Cys	Val	Lys	Gly	Cys	Asp	Leu
				20				25					30		

gct tta gct tct tac tat gta atg cct tta gtt gaa ctc cca act ata
206
Ala Leu Ala Ser Tyr Tyr Val Met Pro Leu Val Glu Leu Pro Thr Ile
35 40 45

aaa aac tat atg caa tca aag ata gtt acc aac tct tct gat gtt tta
254
Lys Asn Tyr Met Gln Ser Lys Ile Val Thr Asn Ser Ser Asp Val Leu
50 55 60

aat agt tac aac aaa gtc tta gta acc aat cat ggt aat att ttt tcc
302
Asn Ser Tyr Asn Lys Val Leu Val Thr Asn His Gly Asn Ile Phe Ser
65 70 75

tat ttt aga atc aac att cca ttc cca tgt gaa tgt att gga ggt gag
350
Tyr Phe Arg Ile Asn Ile Pro Phe Pro Cys Glu Cys Ile Gly Gly Glu
80 85 90 95

ttc tta gga cat gtg ttt gaa tat aca aca aag aaa gga gat act tat
398
Phe Leu Gly His Val Phe Glu Tyr Thr Thr Lys Lys Gly Asp Thr Tyr
100 105 110

gat ttg att gca aat aat tat tat gta agt ttg act agt gtt gag ctt
446
Asp Leu Ile Ala Asn Asn Tyr Tyr Val Ser Leu Thr Ser Val Glu Leu
115 120 125

ttg aag aag ttt aac agc tat gat cca aat cat ata cct gct aag gct
494
Leu Lys Lys Phe Asn Ser Tyr Asp Pro Asn His Ile Pro Ala Lys Ala
130 135 140

aag gtt aat gtt act gtg aat tgt tct tgt ggg aat agc cag att tca
542
Lys Val Asn Val Thr Val Asn Cys Ser Cys Gly Asn Ser Gln Ile Ser
145 150 155

aaa gat tat ggc ttg ttt gtt act tat ccg tta agg tct acg gat tct
590
Lys Asp Tyr Gly Leu Phe Val Thr Tyr Pro Leu Arg Ser Thr Asp Ser
160 165 170 175

ctt gag aag att gcg aac gag tcg aaa ctt gat gaa ggg ttg ata cag
638
Leu Glu Lys Ile Ala Asn Glu Ser Lys Leu Asp Glu Gly Leu Ile Gln
180 185 190

aat ttc aac cct gat gtc aat ttc agt aga gga agt ggg ata gtg ttc
686
Asn Phe Asn Pro Asp Val Asn Phe Ser Arg Gly Ser Gly Ile Val Phe
195 200 205

att cca gga aga gat aaa aat gga gaa tat gtt cct ttg tat cct aaa
734

Ile Pro Gly Arg Asp Lys Asn Gly Glu Tyr Val Pro Leu Tyr Pro Lys
 210 215 220
 aca ggt gtt ggt aag ggt gta gct att ggt ata tct ata gca gga gta
 782
 Thr Gly Val Gly Lys Gly Val Ala Ile Gly Ile Ser Ile Ala Gly Val
 225 230 235
 ttt gcg gtt ctg tta ttt gtt atc tgt ata tat gtc aaa tac ttc cag
 830
 Phe Ala Val Leu Leu Phe Val Ile Cys Ile Tyr Val Lys Tyr Phe Gln
 240 245 250 255
 aaa aag gaa gaa gag aaa act ata ctg ccc caa gtt tct aag gcg ctt
 878
 Lys Lys Glu Glu Glu Lys Thr Ile Leu Pro Gln Val Ser Lys Ala Leu
 260 265 270
 tcg act caa gat ggt aat gcc tcg agt agt gga gaa tat gaa act tca
 926
 Ser Thr Gln Asp Gly Asn Ala Ser Ser Ser Gly Glu Tyr Glu Thr Ser
 275 280 285
 gga tct agt ggg cat ggt act ggt agt gct gca ggc ctc aca gga atc
 974
 Gly Ser Ser Gly His Gly Thr Gly Ser Ala Ala Gly Leu Thr Gly Ile
 290 295 300
 atg gtg gca aag tca act gag ttt tca tat caa gag cta gcc aag gct
 1022
 Met Val Ala Lys Ser Thr Glu Phe Ser Tyr Gln Glu Leu Ala Lys Ala
 305 310 315
 aca gat aac ttt agt ttg gat aat aaa atc ggt caa ggt gga ttt gga
 1070
 Thr Asp Asn Phe Ser Leu Asp Asn Lys Ile Gly Gln Gly Gly Phe Gly
 320 325 330 335
 gct gtc tat tat gca gaa ctc aga ggc gag aaa aca gca atc aag aag
 1118
 Ala Val Tyr Tyr Ala Glu Leu Arg Gly Glu Lys Thr Ala Ile Lys Lys
 340 345 350
 atg aat gtg caa gca tca tca gaa ttt ctg tgt gag ttg aag gtc tta
 1166
 Met Asn Val Gln Ala Ser Ser Glu Phe Leu Cys Glu Leu Lys Val Leu
 355 360 365
 acg cac gtt cat cat ttg aat ctg gtg agg ttg att gga tat tgc gtt
 1214
 Thr His Val His His Leu Asn Leu Val Arg Leu Ile Gly Tyr Cys Val
 370 375 380
 gag ggg tcg ctt ttc ctt gtc tat gaa cat att gac aat gga aac ttg
 1262
 Glu Gly Ser Leu Phe Leu Val Tyr Glu His Ile Asp Asn Gly Asn Leu
 385 390 395

ggt caa tat ttg cat ggt aaa gat aaa gag cca tta cca tgg tct agt
 1310
 Gly Gln Tyr Leu His Gly Lys Asp Lys Glu Pro Leu Pro Trp Ser Ser
 400 405 410 415

aga gtc caa att gct cta gat tca gca cga ggc ctt gaa tac att cat
 1358
 Arg Val Gln Ile Ala Leu Asp Ser Ala Arg Gly Leu Glu Tyr Ile His
 420 425 430

gaa cat acc gtg cct gtg tat atc cat cgc gat gta aaa tca gca aac
 1406
 Glu His Thr Val Pro Val Tyr Ile His Arg Asp Val Lys Ser Ala Asn
 435 440 445

ata ttg ata gac aaa aac ttg cgc gga aag gtt gca gat ttt ggc ttg
 1454
 Ile Leu Ile Asp Lys Asn Leu Arg Gly Lys Val Ala Asp Phe Gly Leu
 450 455 460

acc aaa ctt att gaa gtt gga aat tcc aca ctt cac act cgt ctt gtt
 1502
 Thr Lys Leu Ile Glu Val Gly Asn Ser Thr Leu His Thr Arg Leu Val
 465 470 475

gga act ttt gga tac atg cca cca gaa tat gct caa tat ggt gac gtt
 1550
 Gly Thr Phe Gly Tyr Met Pro Pro Glu Tyr Ala Gln Tyr Gly Asp Val
 480 485 490 495

tct ccg aaa ata gac gta tat gct ttt gga gtt gtt ctt tat gaa ctg
 1598
 Ser Pro Lys Ile Asp Val Tyr Ala Phe Gly Val Val Leu Tyr Glu Leu
 500 505 510

ata tct gca aag aat gct gtt ctg aag aca ggt gaa gaa tct gtt gct
 1646
 Ile Ser Ala Lys Asn Ala Val Leu Lys Thr Gly Glu Glu Ser Val Ala
 515 520 525

gaa tca aag ggt ctt gta gcc ttg ttt gaa aaa gca ctt aat cag att
 1694
 Glu Ser Lys Gly Leu Val Ala Leu Phe Glu Lys Ala Leu Asn Gln Ile
 530 535 540

gat cct tca gaa gct ctt cgc aaa ttg gtg gat cct agg ctt aaa gaa
 1742
 Asp Pro Ser Glu Ala Leu Arg Lys Leu Val Asp Pro Arg Leu Lys Glu
 545 550 555

aac tat cca att gat tct gtt tta aag atg gct caa ctt ggg aga gca
 1790
 Asn Tyr Pro Ile Asp Ser Val Leu Lys Met Ala Gln Leu Gly Arg Ala
 560 565 570 575

tgt aca aga gat aat cca cta cta cgc cca agt atg aga tct tta gtt
1838

Cys Thr Arg Asp Asn Pro Leu Leu Arg Pro Ser Met Arg Ser Leu Val
580 585 590

gtt gat ctt atg aca ctg tca tca cca ttt gaa gat tgt gat gat gac
1886

Val Asp Leu Met Thr Leu Ser Ser Pro Phe Glu Asp Cys Asp Asp Asp
595 600 605

act tcc tat gaa aat caa act ctc ata aat cta ttg tca gtg aga
1931

Thr Ser Tyr Glu Asn Gln Thr Leu Ile Asn Leu Leu Ser Val Arg
610 615 620

tgaaggttct ttgtgccaga ttgaatgatg tttgttaaaa ctgaactagt tgggaagttt
1991

tttactttgt gttcaaagtt tatttcccaa aatgttcaaa aggtcctaga tttcaaaaag
2051

acatcctgta attattttta gtgaagttgt aacactgaag tacaatttgt attatgatgt
2111

gaaaacttta tttttgcttt caaaatgtac ataagataag attctaaac
2160

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<212> PRT
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35 40 45

Asn Tyr Met Gln Ser Lys Ile Val Thr Asn Ser Ser Asp Val Leu Asn
50 55 60

Ser Tyr Asn Lys Val Leu Val Thr Asn His Gly Asn Ile Phe Ser Tyr
65 70 75 80

Phe Arg Ile Asn Ile Pro Phe Pro Cys Glu Cys Ile Gly Gly Glu Phe
85 90 95

Leu Gly His Val Phe Glu Tyr Thr Thr Lys Lys Gly Asp Thr Tyr Asp
100 105 110

Leu Ile Ala Asn Asn Tyr Tyr Val Ser Leu Thr Ser Val Glu Leu Leu
115 120 125

Lys Lys Phe Asn Ser Tyr Asp Pro Asn His Ile Pro Ala Lys Ala Lys
130 135 140

Val Asn Val Thr Val Asn Cys Ser Cys Gly Asn Ser Gln Ile Ser Lys
145 150 155 160

Asp Tyr Gly Leu Phe Val Thr Tyr Pro Leu Arg Ser Thr Asp Ser Leu
165 170 175

Glu Lys Ile Ala Asn Glu Ser Lys Leu Asp Glu Gly Leu Ile Gln Asn
180 185 190

Phe Asn Pro Asp Val Asn Phe Ser Arg Gly Ser Gly Ile Val Phe Ile
195 200 205

Pro Gly Arg Asp Lys Asn Gly Glu Tyr Val Pro Leu Tyr Pro Lys Thr
210 215 220

Gly Val Gly Lys Gly Val Ala Ile Gly Ile Ser Ile Ala Gly Val Phe
225 230 235 240

Ala Val Leu Leu Phe Val Ile Cys Ile Tyr Val Lys Tyr Phe Gln Lys
245 250 255

Lys Glu Glu Glu Lys Thr Ile Leu Pro Gln Val Ser Lys Ala Leu Ser
260 265 270

Thr Gln Asp Gly Asn Ala Ser Ser Ser Gly Glu Tyr Glu Thr Ser Gly
275 280 285

Ser Ser Gly His Gly Thr Gly Ser Ala Ala Gly Leu Thr Gly Ile Met
290 295 300

Val Ala Lys Ser Thr Glu Phe Ser Tyr Gln Glu Leu Ala Lys Ala Thr
305 310 315 320

Asp Asn Phe Ser Leu Asp Asn Lys Ile Gly Gln Gly Gly Phe Gly Ala
325 330 335

Val Tyr Tyr Ala Glu Leu Arg Gly Glu Lys Thr Ala Ile Lys Lys Met
340 345 350

Asn Val Gln Ala Ser Ser Glu Phe Leu Cys Glu Leu Lys Val Leu Thr
355 360 365

His Val His His Leu Asn Leu Val Arg Leu Ile Gly Tyr Cys Val Glu
370 375 380

Gly Ser Leu Phe Leu Val Tyr Glu His Ile Asp Asn Gly Asn Leu Gly
385 390 395 400

Gln Tyr Leu His Gly Lys Asp Lys Glu Pro Leu Pro Trp Ser Ser Arg
405 410 415

Val Gln Ile Ala Leu Asp Ser Ala Arg Gly Leu Glu Tyr Ile His Glu
420 425 430

His Thr Val Pro Val Tyr Ile His Arg Asp Val Lys Ser Ala Asn Ile
435 440 445

Leu Ile Asp Lys Asn Leu Arg Gly Lys Val Ala Asp Phe Gly Leu Thr
450 455 460

Lys Leu Ile Glu Val Gly Asn Ser Thr Leu His Thr Arg Leu Val Gly
465 470 475 480

Thr Phe Gly Tyr Met Pro Pro Glu Tyr Ala Gln Tyr Gly Asp Val Ser
485 490 495

Pro Lys Ile Asp Val Tyr Ala Phe Gly Val Val Leu Tyr Glu Leu Ile
500 505 510

Ser Ala Lys Asn Ala Val Leu Lys Thr Gly Glu Glu Ser Val Ala Glu
515 520 525

Ser Lys Gly Leu Val Ala Leu Phe Glu Lys Ala Leu Asn Gln Ile Asp
530 535 540

Pro Ser Glu Ala Leu Arg Lys Leu Val Asp Pro Arg Leu Lys Glu Asn
 545 550 555 560

Tyr Pro Ile Asp Ser Val Leu Lys Met Ala Gln Leu Gly Arg Ala Cys
 565 570 575

Thr Arg Asp Asn Pro Leu Leu Arg Pro Ser Met Arg Ser Leu Val Val
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 595 600 605

Ser Tyr Glu Asn Gln Thr Leu Ile Asn Leu Leu Ser Val Arg
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 120

ctctttccct tattgattca atg aaa ctc aaa aat ggg tta ctg ctg ttc ttt
 173

Met Lys Leu Lys Asn Gly Leu Leu Leu Phe Phe
 1 5 10

atg ttt ctg gat tgt att ttt ttc aaa gtg gaa tcc aag tgt gta ata
 221

Met Phe Leu Asp Cys Ile Phe Phe Lys Val Glu Ser Lys Cys Val Ile
 15 20 25

ggg tgt gat ata gct tta gct tcc tac tat gta atg cct tta gtt caa
 269

Gly Cys Asp Ile Ala Leu Ala Ser Tyr Tyr Val Met Pro Leu Val Gln
 30 35 40
 ctc tcc aat ata aca acc ttt atg caa tca aag ctt gtt acc aat tct
 317
 Leu Ser Asn Ile Thr Thr Phe Met Gln Ser Lys Leu Val Thr Asn Ser
 45 50 55
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 365
 Phe Glu Val Ile Val Arg Tyr Asn Arg Asp Ile Val Phe Ser Asn Asp
 60 65 70 75
 aat ctt ttt tcc tat ttt aga gtc aac att cca ttc cca tgt gaa tgt
 413
 Asn Leu Phe Ser Tyr Phe Arg Val Asn Ile Pro Phe Pro Cys Glu Cys
 80 85 90
 att gga ggt gaa ttt ctt ggg cat gtg ttt gaa tac act gca aat gaa
 461
 Ile Gly Gly Glu Phe Leu Gly His Val Phe Glu Tyr Thr Ala Asn Glu
 95 100 105
 ggc gat act tat gat tta att gca aat acc tat tat gca agc tta aca
 509
 Gly Asp Thr Tyr Asp Leu Ile Ala Asn Thr Tyr Tyr Ala Ser Leu Thr
 110 115 120
 act gtt gag gtt ttg aaa aag tac aac agc tat gat cca aat cat ata
 557
 Thr Val Glu Val Leu Lys Lys Tyr Asn Ser Tyr Asp Pro Asn His Ile
 125 130 135
 cct gtc aaa gct aag gtt aat gtc act gtt aat tgt tct tgt ggg aac
 605
 Pro Val Lys Ala Lys Val Asn Val Thr Val Asn Cys Ser Cys Gly Asn
 140 145 150 155
 agc cag att tca aaa gac tat ggg cta ttt atc acc tat cca ctt agg
 653
 Ser Gln Ile Ser Lys Asp Tyr Gly Leu Phe Ile Thr Tyr Pro Leu Arg
 160 165 170
 cct agg gat act ctt gag aag att gca aga cat tct aat ctt gat gaa
 701
 Pro Arg Asp Thr Leu Glu Lys Ile Ala Arg His Ser Asn Leu Asp Glu
 175 180 185
 gga gta ata caa agt tac aat ttg ggt gtc aat ttc agc aaa ggc agc
 749
 Gly Val Ile Gln Ser Tyr Asn Leu Gly Val Asn Phe Ser Lys Gly Ser
 190 195 200
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 797
 Gly Val Val Phe Phe Pro Gly Arg Asp Lys Asn Gly Glu Tyr Val Pro
 205 210 215

tta tat cct aga aca ggt ctt ggt aag ggt gca gct gct ggt ata tct
 845
 Leu Tyr Pro Arg Thr Gly Leu Gly Lys Gly Ala Ala Ala Gly Ile Ser
 220 225 230 235

ata gct gga ata ttt gcg ctt ctg tta ttt gtt atc tgc ata tat atc
 893
 Ile Ala Gly Ile Phe Ala Leu Leu Leu Phe Val Ile Cys Ile Tyr Ile
 240 245 250

aaa tac ttc caa aag aag gaa gaa gag aaa act aaa ctg cca caa gtt
 941
 Lys Tyr Phe Gln Lys Lys Glu Glu Glu Lys Thr Lys Leu Pro Gln Val
 255 260 265

tct acg gcg ctt tca gct caa gat gcc tcg ggt agt gga gag tac gaa
 989
 Ser Thr Ala Leu Ser Ala Gln Asp Ala Ser Gly Ser Gly Glu Tyr Glu
 270 275 280

act tcg gga tcc agt ggg cat ggt acc ggt agt act gct ggc ctt aca
 1037
 Thr Ser Gly Ser Ser Gly His Gly Thr Gly Ser Thr Ala Gly Leu Thr
 285 290 295

gga att atg gtg gca aag tca act gag ttt tca tat caa gaa cta gcc
 1085
 Gly Ile Met Val Ala Lys Ser Thr Glu Phe Ser Tyr Gln Glu Leu Ala
 300 305 310 315

aag gct aca aat aac ttc agc tta gat aat aaa att ggt caa ggt gga
 1133
 Lys Ala Thr Asn Asn Phe Ser Leu Asp Asn Lys Ile Gly Gln Gly Gly
 320 325 330

ttt gga gct gtc tat tat gca gta ctc aga ggc gag aaa aca gca att
 1181
 Phe Gly Ala Val Tyr Tyr Ala Val Leu Arg Gly Glu Lys Thr Ala Ile
 335 340 345

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 1229
 Lys Lys Met Asp Val Gln Ala Ser Thr Glu Phe Leu Cys Glu Leu Gln
 350 355 360

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 1277
 Val Leu Thr His Val His His Leu Asn Leu Val Arg Leu Ile Gly Tyr
 365 370 375

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 1325
 Cys Val Glu Gly Ser Leu Phe Leu Val Tyr Glu His Ile Asp Asn Gly
 380 385 390 395

aac ttg ggt caa tat ttg cac ggt ata gat aaa gcg cca tta cca tgg
 1373
 Asn Leu Gly Gln Tyr Leu His Gly Ile Asp Lys Ala Pro Leu Pro Trp
 400 405 410

tca agt agg gtg caa att gct cta gat tcc gca aga ggc ctt gaa tac
 1421
 Ser Ser Arg Val Gln Ile Ala Leu Asp Ser Ala Arg Gly Leu Glu Tyr
 415 420 425

att cat gaa cac act gta cct gtg tat atc cat cgt gat gta aaa tca
 1469
 Ile His Glu His Thr Val Pro Val Tyr Ile His Arg Asp Val Lys Ser
 430 435 440

gcg aat ata tta ata gac aaa aac ttg cac gga aag gtt gca gat ttt
 1517
 Ala Asn Ile Leu Ile Asp Lys Asn Leu His Gly Lys Val Ala Asp Phe
 445 450 455

ggc ttg acc aaa ctt att gaa gtt gga aac tcc aca ctt cac act cgt
 1565
 Gly Leu Thr Lys Leu Ile Glu Val Gly Asn Ser Thr Leu His Thr Arg
 460 465 470 475

cta gtg gga aca ttt gga tac atg cca cca gaa tat gct caa tat ggc
 1613
 Leu Val Gly Thr Phe Gly Tyr Met Pro Pro Glu Tyr Ala Gln Tyr Gly
 480 485 490

gat gtt tct cca aaa ata gat gta tat gct ttt gga gtt gtt ctt tat
 1661
 Asp Val Ser Pro Lys Ile Asp Val Tyr Ala Phe Gly Val Val Leu Tyr
 495 500 505

gag ctt att tct gca aag aat gct att ctg aag aca ggt gaa tct gct
 1709
 Glu Leu Ile Ser Ala Lys Asn Ala Ile Leu Lys Thr Gly Glu Ser Ala
 510 515 520

gtc gaa tca aag ggt ctt gta gca ttg ttt gaa gaa gca ctt aat cag
 1757
 Val Glu Ser Lys Gly Leu Val Ala Leu Phe Glu Glu Ala Leu Asn Gln
 525 530 535

atc gat cct tta gaa gct ctt cgc aaa ttg gtg gat cct agg ctt aaa
 1805
 Ile Asp Pro Leu Glu Ala Leu Arg Lys Leu Val Asp Pro Arg Leu Lys
 540 545 550 555

gaa aac tat cca att gat tct gtt tta aag atg gct caa ctt ggg aga
 1853
 Glu Asn Tyr Pro Ile Asp Ser Val Leu Lys Met Ala Gln Leu Gly Arg
 560 565 570

gca tgt aca aga gac aat cca cta cta cgc cca agt atg aga tct tta
 1901

Ala Cys Thr Arg Asp Asn Pro Leu Leu Arg Pro Ser Met Arg Ser Leu
575 580 585

gtc gtt gct ctt atg aca ctc tta tca cat act gat gat gat gac act
1949

Val Val Ala Leu Met Thr Leu Leu Ser His Thr Asp Asp Asp Asp Thr
590 595 600

ttc tat gaa aat caa tct ctc aca aat cta tta tca gtg aga
1991

Phe Tyr Glu Asn Gln Ser Leu Thr Asn Leu Leu Ser Val Arg
605 610 615

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2051

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2111

tatttcccaa aatagtcaaa aagtcctaga tccaaagaag acatcctgta attattttta
2171

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2217

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<400> 54

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Leu Ala Ser Tyr Tyr Val Met Pro Leu Val Gln Leu Ser Asn Ile Thr
35 40 45

Thr Phe Met Gln Ser Lys Leu Val Thr Asn Ser Phe Glu Val Ile Val
50 55 60

Arg Tyr Asn Arg Asp Ile Val Phe Ser Asn Asp Asn Leu Phe Ser Tyr
65 70 75 80

Phe Arg Val Asn Ile Pro Phe Pro Cys Glu Cys Ile Gly Gly Glu Phe
85 90 95

Leu Gly His Val Phe Glu Tyr Thr Ala Asn Glu Gly Asp Thr Tyr Asp
100 105 110

Leu Ile Ala Asn Thr Tyr Tyr Ala Ser Leu Thr Thr Val Glu Val Leu
115 120 125

Lys Lys Tyr Asn Ser Tyr Asp Pro Asn His Ile Pro Val Lys Ala Lys
130 135 140

Val Asn Val Thr Val Asn Cys Ser Cys Gly Asn Ser Gln Ile Ser Lys
145 150 155 160

Asp Tyr Gly Leu Phe Ile Thr Tyr Pro Leu Arg Pro Arg Asp Thr Leu
165 170 175

Glu Lys Ile Ala Arg His Ser Asn Leu Asp Glu Gly Val Ile Gln Ser
180 185 190

Tyr Asn Leu Gly Val Asn Phe Ser Lys Gly Ser Gly Val Val Phe Phe
195 200 205

Pro Gly Arg Asp Lys Asn Gly Glu Tyr Val Pro Leu Tyr Pro Arg Thr
210 215 220

Gly Leu Gly Lys Gly Ala Ala Ala Gly Ile Ser Ile Ala Gly Ile Phe
225 230 235 240

Ala Leu Leu Leu Phe Val Ile Cys Ile Tyr Ile Lys Tyr Phe Gln Lys
245 250 255

Lys Glu Glu Glu Lys Thr Lys Leu Pro Gln Val Ser Thr Ala Leu Ser
260 265 270

Ala Gln Asp Ala Ser Gly Ser Gly Glu Tyr Glu Thr Ser Gly Ser Ser
275 280 285

Gly His Gly Thr Gly Ser Thr Ala Gly Leu Thr Gly Ile Met Val Ala
290 295 300

Lys Ser Thr Glu Phe Ser Tyr Gln Glu Leu Ala Lys Ala Thr Asn Asn
305 310 315 320

Phe Ser Leu Asp Asn Lys Ile Gly Gln Gly Gly Phe Gly Ala Val Tyr

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Tyr	Ala	Val	Leu	Arg	Gly	Glu	Lys	Thr	Ala	Ile	Lys	Lys	Met	Asp	Val
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Gln	Ala	Ser	Thr	Glu	Phe	Leu	Cys	Glu	Leu	Gln	Val	Leu	Thr	His	Val
		355					360					365			
His	His	Leu	Asn	Leu	Val	Arg	Leu	Ile	Gly	Tyr	Cys	Val	Glu	Gly	Ser
	370					375					380				
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385					390					395				400	
Leu	His	Gly	Ile	Asp	Lys	Ala	Pro	Leu	Pro	Trp	Ser	Ser	Arg	Val	Gln
				405					410					415	
Ile	Ala	Leu	Asp	Ser	Ala	Arg	Gly	Leu	Glu	Tyr	Ile	His	Glu	His	Thr
			420					425					430		
Val	Pro	Val	Tyr	Ile	His	Arg	Asp	Val	Lys	Ser	Ala	Asn	Ile	Leu	Ile
		435					440					445			
Asp	Lys	Asn	Leu	His	Gly	Lys	Val	Ala	Asp	Phe	Gly	Leu	Thr	Lys	Leu
	450					455					460				
Ile	Glu	Val	Gly	Asn	Ser	Thr	Leu	His	Thr	Arg	Leu	Val	Gly	Thr	Phe
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Gly	Tyr	Met	Pro	Pro	Glu	Tyr	Ala	Gln	Tyr	Gly	Asp	Val	Ser	Pro	Lys
				485					490					495	
Ile	Asp	Val	Tyr	Ala	Phe	Gly	Val	Val	Leu	Tyr	Glu	Leu	Ile	Ser	Ala
		500						505					510		
Lys	Asn	Ala	Ile	Leu	Lys	Thr	Gly	Glu	Ser	Ala	Val	Glu	Ser	Lys	Gly
	515						520					525			
Leu	Val	Ala	Leu	Phe	Glu	Glu	Ala	Leu	Asn	Gln	Ile	Asp	Pro	Leu	Glu
	530					535					540				
Ala	Leu	Arg	Lys	Leu	Val	Asp	Pro	Arg	Leu	Lys	Glu	Asn	Tyr	Pro	Ile
545					550					555				560	

Asp Ser Val Leu Lys Met Ala Gln Leu Gly Arg Ala Cys Thr Arg Asp
565 570 575

Asn Pro Leu Leu Arg Pro Ser Met Arg Ser Leu Val Val Ala Leu Met
580 585 590

Thr Leu Leu Ser His Thr Asp Asp Asp Asp Thr Phe Tyr Glu Asn Gln
595 600 605

Ser Leu Thr Asn Leu Leu Ser Val Arg
610 615